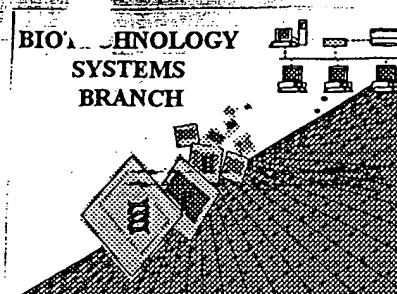


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/680,121

Source: OIPE

Date Processed by STIC: 10-18-00

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/680,121

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☒ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) ____ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

Does Not Comply
Corrected Diskette Needed
see p. 6

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/680,121
 DATE: 10/18/2000
 TIME: 17:20:29

Input Set : A:\Mueth31.app
 Output Set: N:\CRF3\10182000\I680121.raw

```

71 aag aat tca ttg cat ctg gat ctt gaa aag aga gat ctc aat ggc aat 462
72 Lys Asn Ser Leu His Leu Asp Leu Glu Lys Arg Asp Leu Asn Gly Asn
73 90 95 100
75 ttt ccc aaa acc aac ctc aaa cct ggc agt cct tct gat ctg gag aat 510
76 Phe Pro Lys Thr Asn Leu Lys Pro Gly Ser Pro Ser Asp Leu Glu Asn
77 105 110 115 120
79 gca acc ccg aag ctc ttt tta gaa ggg gaa aaa gag tca gtt tcc cct 558
80 Ala Thr Pro Lys Leu Phe Leu Glu Gly Glu Lys Glu Ser Val Ser Pro
81 125 130 135
83 gag agt tta aag tcc agc act tcc ctt act tca gaa gag aaa caa gag 606
84 Glu Ser Leu Lys Ser Ser Thr Ser Leu Thr Ser Glu Glu Lys Gln Glu
85 140 145 150
87 aag ctg gga act ctc ttc ttc tcc tta gaa tac aac ttc gag aga aaa 654
88 Lys Leu Gly Thr Leu Phe Phe Ser Leu Glu Tyr Asn Phe Glu Arg Lys
89 155 160 165
91 gca ttt gtg gtc aat atc aag gaa gcc cgt ggc ttg cca gcc atg gat 702
92 Ala Phe Val Val Asn Ile Lys Glu Ala Arg Gly Leu Pro Ala Met Asp
93 170 175 180
95 gag cag tcg atg acc tct gac cca tat atc aaa atg acg atc ctc cca 750
96 Glu Gln Ser Met Thr Ser Asp Pro Tyr Ile Lys Met Thr Ile Leu Pro
97 185 190 195 200
99 gag aag aag cat aaa gtg aaa act aga gtg ctg aga aaa acc ttg gat 798
100 Glu Lys Lys His Lys Val Lys Thr Arg Val Leu Arg Lys Thr Leu Asp
101 205 210 215
103 cca gct ttt gat gag acc ttt aca ttc tat ggg ata ccc tac acc caa 846
104 Pro Ala Phe Asp Glu Thr Phe Thr Phe Tyr Gly Ile Pro Tyr Thr Gln
105 220 225 230
107 atc caa gaa ttg gcc ttg cac ttc aca att ttg agt ttt gac agg ttt 894
108 Ile Gln Glu Leu Ala Leu His Phe Thr Ile Leu Ser Phe Asp Arg Phe
109 235 240 245
111 tca aga gat gat atc att ggg gaa gtt cta att cct ctc tcg gga att 942
112 Ser Arg Asp Asp Ile Ile Gly Glu Val Leu Ile Pro Leu Ser Gly Ile
113 250 255 260
115 gaa tta tct gaa gga aaa atg tta atg aat aga gag atc atc aag aga 990
116 Glu Leu Ser Glu Gly Lys Met Leu Met Asn Arg Glu Ile Ile Lys Arg
117 265 270 275 280
119 aat gtt agg aag tct tca gga cgg ggt gag tta ctg atc tct ctc tgc 1038
120 Asn Val Arg Lys Ser Ser Gly Arg Gly Glu Leu Leu Ile Ser Leu Cys
121 285 290 295
123 tat cag tcc acc aca aac act cta act gtg gtt gtc tta aaa gct cga 1086
124 Tyr Gln Ser Thr Thr Asn Thr Leu Thr Val Val Val Leu Lys Ala Arg
125 300 305 310
127 cat ctg cct aaa tct gat gtg tcc gga ctt tca gat ccc tat gtc aaa 1134
128 His Leu Pro Lys Ser Asp Val Ser Gly Leu Ser Asp Pro Tyr Val Lys
129 315 320 325
131 gtg aac ctg tac cat gcc aaa aag aga atc tcc aag aag aag act cat 1182
132 Val Asn Leu Tyr His Ala Lys Lys Arg Ile Ser Lys Lys Lys Thr His
133 330 335 340
135 gtg aag aaa tgc acc ccc aat gca gtg ttc aat gag ctg ttt gtc ttt 1230

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RAW SEQUENCE LISTING

DATE: 10/18/2000

PATENT APPLICATION: US/09/680,121

TIME: 17:20:29

Input Set : A:\Mueth31.app

Output Set: N:\CRF3\10182000\I680121.raw

```

136 Val Lys Lys Cys Thr Pro Asn Ala Val Phe Asn Glu Leu Phe Val Phe
137 345 350 355 360
139 gat att cct tgt gag ggc ctt gaa gat ata agt gtt gaa ttt ttg gtt 1278
140 Asp Ile Pro Cys Glu Gly Leu Glu Asp Ile Ser Val Glu Phe Leu Val
141 365 370 375
143 ttg gat tct gaa agg ggg tcc cga aat gag gta atc ggg cag tta gtc 1326
144 Leu Asp Ser Glu Arg Gly Ser Arg Asn Glu Val Ile Gly Gln Leu Val
145 380 385 390
147 ttg ggt gca gca gca gaa gga act ggt gga gag cac tgg aaa gag atc 1374
148 Leu Gly Ala Ala Ala Glu Gly Thr Gly Gly Glu His Trp Lys Glu Ile
149 395 400 405
151 tgt gac tac ccc agg aga caa att gcc aag tgg cac gtg ctc tgt gat 1422
152 Cys Asp Tyr Pro Arg Arg Gln Ile Ala Lys Trp His Val Leu Cys Asp
153 410 415 420
155 ggt tagcatccta gccgtgagtt ggaacttaaa ggtttttact aggcaaggag 1475
156 Gly
157 425
159 aaatthttctt tttttctata ttggattgca agcttgggaa atcaagctac ctttttgttg 1535
161 ttgttgttgt tgctagaaat ggattgaatt agtagaccag aaagtaactt caaatgtgta 1595
163 ttatgataat ttccctattt attagaagag ttggataaat ttccataaga tattcaatat 1655
165 ctcccttcaga ttaccagtga tataactagg aatagtcaga ctttttatga atactgtgcc 1715
167 agaateccaa attataaatg tgacaatctc attggaacat gtcacaaaaa gttaattgtga 1775
169 ttaagattta aaaacgaaaa gtatgccttg cttgttgaaa atttatccat ttatcttcag 1835
171 gttgggggaa atcaatthttt ctttaactca aagatactaa aaaaatgtcc tccagtthgt 1895
173 atttattaat tctgtcatgt gcaaatgggt gtccctgcata taaaagtatc tgggtcatttc 1955
175 agtttgggttt gtaattattt gatgcaattt tatcataaga gtaactcaga ttcatttcaa 2015
177 aaggacagtg aacaagctga gaaattattt tatcaaaggg ctgagttgag aacactgtgg 2075
179 ctgaaatata atthttctcc ccctaaaggt tacatgtgag tcaaatthtt gtaaaatata 2135
181 acctcacata agaaccatgg ccttggtatta ttcactgcct gtcacaagcc tcagtgtggc 2195
183 ctgagaaatc cctatgtacc tttgtgaaat tgttgaatta gttagtgaat aaagaaataa 2255
185 acttcaacta gaaatccagt tagaagtga atthttctat aggaaatagg tatagtgtgc 2315
187 aagtgtactt ttaaggccat cgtttgtacc cagagtccgc atggccacct aagtcttcat 2375
189 ttaatttatt gtcccccaga aaagattaag atgctacttg aaaagactgt gaagatttht 2435
191 tacattgcca gataaaaagt gttacttaac caacaaacaa atgtaagact acaaaatcgt 2495
193 tcaagagcaa ttctaatata atttacatat gtccacgcaa aatatgctta ggctgtcaaa 2555
195 ttagcacaac aaagaatgtg tttcactatc tttctatagg taatttgtct tgagctgttg 2615
197 tctatagagc agttttacaga cttgtgtctt gtatcatttt ccagtgccag ggttctgaaa 2675
199 ttcattcaga acctgttaga ttaaagctgc accctgtgat ttttgaaaa gaattagctt 2735
201 gagagtaatg tcaactatatt tgagttctta gagaagtatg agtggaaact gagtacagtt 2795
203 gaattattaa atatgcaagt tagaaaattaa gtctactgaa aaatttacat tttgagtcag 2855
205 gttttgtgtc agtactttag cagtttttga gaatgtgttt gatatcacag tgtttgtaaa 2915
207 ttctatgaaa aatgcatttt ccaaacaact tatcatgct ttttatgact atgcctaatt 2975
209 taaagaaaaa gtattacatt ctgtatgtac aaagattaaa aatcaacctc ttttttgtgc 3035
211 tttaaaatga ctttgggatt aaaaaagcat atthcccaat cattgtcttc attccactac 3095
213 aaagtcacct cacagcatct tgctccactc ggcactctct tgaaagcaac atgaaatgaa 3155
215 ctgtagtagg tgtgtagttt ggggaagtca aatggccatt ttatgtatgt gcatttggtg 3215
217 tcatgggccc tggaacagaa tatatgttgg acctctgaaa agttgttaagg ggccaaatct 3275
219 aagtattctt cacggcagcc agaagttaat ggtggttagc gctgaggtat ggttgttggg 3335
221 cgaggccgat tttttttttt taacatggaa caatgaaacc aacaacaaac atthtttaaa 3395

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/680,121

DATE: 10/18/2000

TIME: 17:20:29

Input Set : A:\Mueth31.app

Output Set : N:\CRF3\10182000\I680121.raw

```

223 ttaaaatgga taatttgtaa atagttttta gcttttaaaa tttaaagtgt ttttgagtgt 3455
225 gaaaagtga gtaaaactat ttgcaactgg ttttcagaaa agagaaaaga aacaacaaag 3515
227 gaattgaaac aggcaggag atcttaatac ctaatttcac catttctgca aaatgtactg 3575
229 ttttagaatg tattacaata tcaatgtgaa tatcttgaat cctgttacaa atcctgcact 3635
231 gtattaaaca tgtaaattaa ttgtttgtct gattagccaa tctcaccacc caaatgggga 3695
233 ggtatacatg tttgaagaac gtgtaactcg gtaattgatt tggtctgatg ttgtaactca 3755
235 atagaagtgt tttggaagga agcatggtgt gtgagacagt gtctgttctt ttgtgccagc 3815
237 tctgtatgat gttgtgaaga ccatgtttgt aagacatgaa taaattgctg cttttgccca 3875
239 aaaaaaaaaa aaaaaa 3891
242 <210> SEQ ID NO: 2
243 <211> LENGTH: 425
244 <212> TYPE: PRT
245 <213> ORGANISM: Homo sapiens
246 <223> OTHER INFORMATION: product = Repro-PC-1.0
248 <400> SEQUENCE: 2
249 Met Ala Pro Ile Thr Thr Ser Arg Glu Glu Phe Asp Glu Ile Pro Thr
250 1 5 10 15
252 Val Val Gly Ile Phe Ser Ala Phe Gly Leu Val Phe Thr Val Ser Leu
253 20 25 30
255 Phe Ala Trp Ile Cys Cys Gln Arg Lys Ser Ser Lys Ser Asn Lys Thr
256 35 40 45
258 Pro Pro Tyr Lys Phe Val His Val Leu Lys Gly Val Asp Ile Tyr Pro
259 50 55 60
261 Glu Asn Leu Asn Ser Lys Lys Phe Gly Ala Asp Asp Lys Asn Glu
262 65 70 75 80
264 Val Lys Asn Lys Pro Ala Val Pro Lys Asn Ser Leu His Leu Asp Leu
265 85 90 95
267 Glu Lys Arg Asp Leu Asn Gly Asn Phe Pro Lys Thr Asn Leu Lys Pro
268 100 105 110
270 Gly Ser Pro Ser Asp Leu Glu Asn Ala Thr Pro Lys Leu Phe Leu Glu
271 115 120 125
273 Gly Glu Lys Glu Ser Val Ser Pro Glu Ser Leu Lys Ser Ser Thr Ser
274 130 135 140
276 Leu Thr Ser Glu Glu Lys Gln Glu Lys Leu Gly Thr Leu Phe Phe Ser
277 145 150 155 160
279 Leu Glu Tyr Asn Phe Glu Arg Lys Ala Phe Val Val Asn Ile Lys Glu
280 165 170 175
282 Ala Arg Gly Leu Pro Ala Met Asp Glu Gln Ser Met Thr Ser Asp Pro
283 180 185 190
285 Tyr Ile Lys Met Thr Ile Leu Pro Glu Lys Lys His Lys Val Lys Thr
286 195 200 205
288 Arg Val Leu Arg Lys Thr Leu Asp Pro Ala Phe Asp Glu Thr Phe Thr
289 210 215 220
291 Phe Tyr Gly Ile Pro Tyr Thr Gln Ile Gln Glu Leu Ala Leu His Phe
292 225 230 235 240
294 Thr Ile Leu Ser Phe Asp Arg Phe Ser Arg Asp Asp Ile Ile Gly Glu
295 245 250 255
297 Val Leu Ile Pro Leu Ser Gly Ile Glu Leu Ser Glu Gly Lys Met Leu
298 260 265 270

```

09/680, 121

P.6

<210> 11 Seg # 11

<211> 9

<212> PRT

<213> Homo sapiens

<220>

<223> residue 1=Thr, Ser or Met

<220>

<223> residue 2=Asp, Glu, Ala, Ser or Thr

<400> 11

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr
1 5

OK

↓
All "Xaa's" in the sequence
must be explained. See #10
on Error Summary Sheet.

This error is indicated throughout
the sequence listing.

← F.Y.I.

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 10/18/2000

PATENT APPLICATION: US/09/680,121

TIME: 17:20:30

Input Set : A:\Mueth31.app

Output Set: N:\CRF3\10182000\I680121.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:648 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:11
L:648 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:648 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11
L:664 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12
L:664 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12
L:664 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:12
L:677 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:677 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:677 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:13
L:690 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:14
L:690 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14
L:690 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:14
L:707 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:15
L:707 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15
L:707 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
L:724 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:16
L:724 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:724 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:16
L:737 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17
L:737 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:737 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:17
L:750 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:18
L:750 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:18
L:750 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18
L:766 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:19
L:766 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:19
L:766 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:19
L:779 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:20
L:779 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20
L:779 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:20
L:885 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:27
L:885 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:885 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:27



Creation date: 12-20-2003
Indexing Officer: TBUI1 - THU-TRANG BUI
Team: OIPEBackFileIndexing
Dossier: 09680121

Legal Date: 11-11-2002

No.	Doccode	Number of pages
1	C.AD	1

Total number of pages: 1

Remarks:

Order of re-scan issued on